

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
- (ii) TITLE OF INVENTION: Novel CREBa Isoform
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: Januray 12, 1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Williams Jr., Joseph A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/33469
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-474-6300
 - (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 304..1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTGG CTCCTTTTG GATGCACAGC	60
CCGATTTAAC CCCTGCACCT TCCGCCCAGT CCCAGCAGGC TTGTCCTCCC CGGGGAGTCA	120
CAGATTTCCG AGGACAAGGG TCGCGTAGCC TTCGGCAGGG CTCTCCCGAG TTCCTGCTCC	180
AGTGCATAAG TTCCACGCGC GCACACGCCA AGTACACGGG GAGAAGCGTC TCACCGGCCC	240
GCGGCGGCTC TGCGCGGTCC CCTCCTGCCT CAGCATCCTC GGGCCTGCGC GGCGCCCACC	300
GCC ATG GAG GTG CTG GAG AGC GGG GAG CAG AGC GTC CTG CAG TGG GAC	348
Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp	
1 5 10 15	
CGC AAG CTG AGC GAG CTG TCA GAG CCC GGA GAG ACT GAG GCC CTC ATG	396
Arg Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met	
20 25 30	
TAC CAC ACG CAC TTC TCG GAG CTC CTA GAC GAG TTT TCC CAG AAC GTC	444
Tyr His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val	
35 40 45	
CTG GGT CAG CTC CTG AGT GAC CCT TTC CTC TCA GAG AAG AGC GAG TCA	492
Leu Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser	
50 55 60	
ATG GAG GTG GAG CCA TCT CCA ACA TCA CCA GCG CCT CTC ATC CAG GCT	540
Met Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala	
65 70 75	
GAA CAC AGC TAC TCT CTG AGC GAG GAG CCC CGG ACT CAG TCA CCA TTT	588
Glu His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe	
80 85 90 95	
ACC CAT GCG GCT ACC AGC GAC AGC TTC AAT GAC GAG GAG GTG GAG AGT	636
Thr His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser	
100 105 110	
GAA AAA TGG TAC CTG TCT ACA GAG TTT CCT TCA GCT ACC ATC AAG AAA	684
Glu Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys	
115 120 125	
GAG CCA ATC ACA GAG GAG CAG CCC CCG GGA CTT GTC CCT TCT GTC ACT	732
Glu Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr	
130 135 140	
CTG ACC ATC ACA GCC ATT TCC ACT CCT TTT GAA AAA GAA GAG TCC CCT	780
Leu Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro	
145 150 155	
CTG GAT ATG AAT GCT GGG GGG GAC TCC TCA TGC CAG ACG CTT ATT CCT	828

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Leu	Asp	Met	Asn	Ala	Gly	Gly	Asp	Ser	Ser	Cys	Gln	Thr	Leu	Ile	Pro	
160					165					170					175	
AAG	ATT	AAG	CTG	GAG	CCC	CAC	GAA	GTG	GAT	CAG	TTC	TTA	AAC	TTC	TCC	876
Lys	Ile	Lys	Leu	Glu	Pro	His	Glu	Val	Asp	Gln	Phe	Leu	Asn	Phe	Ser	
				180					185					190		
CCG	AAA	GAA	GCC	TCC	GTG	GAT	CAA	CTG	CAC	TTA	CCA	CCA	ACA	CCA	CCC	924
Pro	Lys	Glu	Ala	Ser	Val	Asp	Gln	Leu	His	Leu	Pro	Pro	Thr	Pro	Pro	
			195					200					205			
AGT	AGT	CAC	AGC	AGT	GAC	TCT	GAG	GGC	AGC	TTG	AGC	CCC	AAC	CCA	CGC	972
Ser	Ser	His	Ser	Ser	Asp	Ser	Glu	Gly	Ser	Leu	Ser	Pro	Asn	Pro	Arg	
		210					215					220				
CTG	CAT	CCC	TTC	AGC	CTG	TCT	CAG	GCC	CAC	AGC	CCT	GTC	AGA	GCC	ATG	1020
Leu	His	Pro	Phe	Ser	Leu	Ser	Gln	Ala	His	Ser	Pro	Val	Arg	Ala	Met	
	225					230					235					
CCC	CGG	GGC	CCC	TCT	GCC	TTG	TCC	ACA	TCT	CCT	CTC	CTC	ACA	GCT	CCA	1068
Pro	Arg	Gly	Pro	Ser	Ala	Leu	Ser	Thr	Ser	Pro	Leu	Leu	Thr	Ala	Pro	
240					245					250					255	
CAT	AAG	CTG	CAG	GGA	TCG	GGC	CCC	CTG	GTC	CTG	ACA	GAA	GAG	GAG	AAG	1116
His	Lys	Leu	Gln	Gly	Ser	Gly	Pro	Leu	Val	Leu	Thr	Glu	Glu	Glu	Lys	
			260						265				270			
AGG	ACC	CTG	GTT	GCC	GAG	GGC	TAT	CCC	ATT	CCC	ACC	AAG	CTG	CCT	CTG	1164
Arg	Thr	Leu	Val	Ala	Glu	Gly	Tyr	Pro	Ile	Pro	Thr	Lys	Leu	Pro	Leu	
			275					280					285			
ACA	AAA	TCT	GAG	GAG	AAG	GCC	CTG	AAG	AAA	ATC	CGG	AGA	AAG	ATC	AAG	1212
Thr	Lys	Ser	Glu	Glu	Lys	Ala	Leu	Lys	Lys	Ile	Arg	Arg	Lys	Ile	Lys	
		290					295					300				
AAT	AAG	ATT	TCT	GCC	CAA	GAA	AGC	AGG	AGA	AAG	AAG	AAA	GAA	TAC	ATG	1260
Asn	Lys	Ile	Ser	Ala	Gln	Glu	Ser	Arg	Arg	Lys	Lys	Lys	Glu	Tyr	Met	
	305					310					315					
GAC	AGC	CTG	GAG	AAA	AAA	GTG	GAG	TCT	TGT	TCA	ACT	GAG	AAC	TTG	GAG	1308
Asp	Ser	Leu	Glu	Lys	Lys	Val	Glu	Ser	Cys	Ser	Thr	Glu	Asn	Leu	Glu	
320					325					330					335	
CTT	CGG	AAG	AAG	GTG	GAG	GTG	CTG	GAG	AAC	ACC	AAT	AGG	ACT	CTC	CTT	1356
Leu	Arg	Lys	Lys	Val	Glu	Val	Leu	Glu	Asn	Thr	Asn	Arg	Thr	Leu	Leu	
			340						345					350		
CAG	CAA	CTT	CAG	AAG	CTT	CAG	ACT	TTG	GTG	ATG	GGG	AAG	GTC	TCT	CGA	1404
Gln	Gln	Leu	Gln	Lys	Leu	Gln	Thr	Leu	Val	Met	Gly	Lys	Val	Ser	Arg	
			355				360					365				
ACC	TGC	AAG	TTA	GCT	GGC	ACA	CAG	ACT	GGC	ACC	TGC	CTC	ATG	GTC	GTT	1452
Thr	Cys	Lys	Leu	Ala	Gly	Thr	Gln	Thr	Gly	Thr	Cys	Leu	Met	Val	Val	

GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly 385 390 395	1500
CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu 400 405 410 415	1548
TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile 420 425 430	1596
TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG TCG AGC CCA GCC TCA ACC Tyr Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr 435 440 445	1644
GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG Gly Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser 450 455 460	1692
TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile 465 470 475	1740
TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln 480 485 490 495	1788
CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val 500 505 510	1836
GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCTCC Glu Leu Glu Arg Arg Val Asn Ala Thr Phe 515 520	1886
TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTTCCCC TTCACCACTG GATCTCGAGG	1946
AGGAGATGGC TAGTGTTACG GCTCGAGACA GGAGGCCAGC CCAGGGGGTT CTGCTTATGT	2006
GTCCCCGTGG CTCTCCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTTCT CTTACTGCCA	2066
TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTTT CCACCAATAG	2126
TGCCAAGAAG AACTGCCTG ATTCTTCCCC GGGAGGAGTG ACTCCTCTGA AGAAGACATG	2186
ACTCATGTTC AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA	2246
GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCTGCAC	2306
TGAGAGGACC AAAGCGTCAT TGCAGTCTTC TCTCCACCCT GTACCCCGGA GTCCTGATTG	2366
GATGTCTGCA GAGGCAGATG GGGCTCCAC CATATTTTCA GGCCGCAAGT GCAATTCTCTG	2426

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AAGGCATCAG GCTCTTCTCT CCCAGGCTCT CCTGCCCACT GTGTTGTTTG TAGGACACCC 2486
 CCACACCCAC TCATACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT 2546
 CCCCTCCCCA TTTGTAAATA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG 2606
 AAAAGATTTT CCCTTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGGAACA GGAGAGTCCC 2666
 CGGAATCTAG GACCCTAGTC TTTGTACTTG ATGCCTTGTT TCCCCCCTTT TCTTCTTTAA 2726
 AATTGGGGAC CTATAACATC ATCGCTGTTG CGGAATCCAC TTAGGCATGT GTCCCCTGAT 2786
 GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT 2846
 TCCTCTCTCT GGTCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG 2906
 ACACCCTTGC TAGCTTGTC TGCCTACCTG CTTACCCAC TCCCTCACCT TCCTCCTTCC 2966
 CTTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTTGTAC 3026
 ACCCACAGTG GTACCTTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA 3086
 TAACTAAACC CTAAACTCTT TTTTGTGTGT TGTGTGTGTT GTTTTTTTTT TTTATGATTA 3146
 AAAAGTAAAA ATTGTAGTTT AAAAAAAAAA AAAAAAACT CGAG 3190

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg
 1 5 10 15
 Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr
 20 25 30
 His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
 35 40 45
 Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met
 50 55 60
 Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
 65 70 75 80
 His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr

85	90	95
His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu		
100	105	110
Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu		
115	120	125
Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu		
130	135	140
Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu		
145	150	155
Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys		
165	170	175
Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro		
180	185	190
Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser		
195	200	205
Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu		
210	215	220
His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro		
225	230	235
Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His		
245	250	255
Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg		
260	265	270
Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr		
275	280	285
Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn		
290	295	300
Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp		
305	310	315
Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu		
325	330	335
Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln		
340	345	350
Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr		
355	360	365
Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val		

098456-064901

370	375	380
Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro		
385	390	395 400
Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser		
	405	410 415
Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr		
	420	425 430
Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly		
	435	440 445
Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser		
	450	455 460
Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser		
	465	470 475 480
Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His		
	485	490 495
Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu		
	500	505 510
Leu Glu Arg Arg Val Asn Ala Thr Phe		
	515	520

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCT AATGGAGCTG AGAGTCGGG

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCG CTCATCGGTG CACGACAGA

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ACAGCTCCAC ATAAGCTGC

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAATTCGCT CAAGGAGAGT CCTATTGG

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGTCAGTT CAGCGGATCC TGTCGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
NNNNNNNNNG AGGCGAATTC AGTGCAACTG CAGC 154

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTCAGTT CAGCGGATCC TGTCG 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCAGTTG CACTGAATTC GCCTC 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

058456-064901

- 34 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATCGGGCC GCCGAGATCT CATATGGAGC TGAGAGTC

38

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